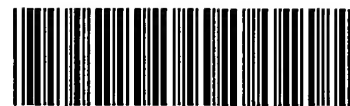


RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/535,325
Source: 1 FWP
Date Processed by STIC: 7/31/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 07/31/2006

PATENT APPLICATION: US/10/535,325

TIME: 14:19:29

Input Set : A:\TSRI6516SEQ.TXT

Output Set: N:\CRF4\07312006\J535325.raw

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4 <110> APPLICANT: The Scripps Research Institute
5     Cheresch, David A.
6     Paul, Robert
7     Eliceiri, Brian
9 <120> TITLE OF INVENTION: Method of Treatment of Myocardial
10    Infarction
12 <130> FILE REFERENCE: TSRI-651.6
14 <140> CURRENT APPLICATION NUMBER: 10/535,325
15 <141> CURRENT FILING DATE: 2005-05-18
17 <150> PRIOR APPLICATION NUMBER: 10/298,377
18 <151> PRIOR FILING DATE: 2002-11-18
20 <150> PRIOR APPLICATION NUMBER: 09/538,248
21 <151> PRIOR FILING DATE: 2000-03-29
23 <150> PRIOR APPLICATION NUMBER: 09/470,881
24 <151> PRIOR FILING DATE: 1999-12-22
26 <150> PRIOR APPLICATION NUMBER: PCT/US99/11780
27 <151> PRIOR FILING DATE: 1999-05-28
29 <150> PRIOR APPLICATION NUMBER: 60/087,220
30 <151> PRIOR FILING DATE: 1998-05-29
32 <160> NUMBER OF SEQ ID NOS: 4
34 <170> SOFTWARE: FastSEQ for Windows Version 4.0
36 <210> SEQ ID NO: 1
37 <211> LENGTH: 2187
38 <212> TYPE: DNA
39 <213> ORGANISM: homo sapiens
41 <220> FEATURE:
42 <221> NAME/KEY: CDS
43 <222> LOCATION: (134)...(1486)
45 <400> SEQUENCE: 1
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47 caagagagct ctaatggtac caagtgcacag gttggcttta ctgtgactcg gggacgccag 120
48 agctcctgag aag atg tca gca ata cag gcc gcc tgg cca tcc ggt aca 169
49             Met Ser Ala Ile Gln Ala Ala Trp Pro Ser Gly Thr
50             1             5             10
52 gaa tgt att gcc aag tac aac ttc cac ggc act gcc gag cag gac ctg 217
53 Glu Cys Ile Ala Lys Tyr Asn Phe His Gly Thr Ala Glu Gln Asp Leu
54             15             20             25
56 ccc ttc tgc aaa gga gac gtg ctc acc att gtg gcc gtc acc aag gac 265
57 Pro Phe Cys Lys Gly Asp Val Leu Thr Ile Val Ala Val Thr Lys Asp
58             30             35             40
60 ccc aac tgg tac aaa gcc aaa aac aag gtg ggc cgt gag ggc atc atc 313
61 Pro Asn Trp Tyr Lys Ala Lys Asn Lys Val Gly Arg Glu Gly Ile Ile
62 45             50             55             60

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64 cca gcc aac tac gtc cag aag cgg gag ggc gtg aag gcg ggt acc aaa 361
65 Pro Ala Asn Tyr Val Gln Lys Arg Glu Gly Val Lys Ala Gly Thr Lys
66                               65                               70                               75
68 ctc agc ctc atg cct tgg ttc cac ggc aag atc aca cgg gag cag gct 409
69 Leu Ser Leu Met Pro Trp Phe His Gly Lys Ile Thr Arg Glu Gln Ala
70                               80                               85                               90
72 gag cgg ctt ctg tac ccg ccg gag aca ggc ctg ttc ctg gtg cgg gag 457
73 Glu Arg Leu Leu Tyr Pro Pro Glu Thr Gly Leu Phe Leu Val Arg Glu
74                               95                               100                               105
76 agc acc aac tac ccc gga gac tac acg ctg tgc gtg agc tgc gac ggc 505
77 Ser Thr Asn Tyr Pro Gly Asp Tyr Thr Leu Cys Val Ser Cys Asp Gly
78                               110                               115                               120
80 aag gtg gag cac tac cgc atc atg tac cat gcc agc aag ctc agc atc 553
81 Lys Val Glu His Tyr Arg Ile Met Tyr His Ala Ser Lys Leu Ser Ile
82 125                               130                               135                               140
84 gac gag gag gtg tac ttt gag aac ctc atg cag ctg gtg gag cac tac 601
85 Asp Glu Glu Val Tyr Phe Glu Asn Leu Met Gln Leu Val Glu His Tyr
86                               145                               150                               155
88 acc tca gac gca gat gga ctc tgt acg cgc ctc att aaa cca aag gtc 649
89 Thr Ser Asp Ala Asp Gly Leu Cys Thr Arg Leu Ile Lys Pro Lys Val
90                               160                               165                               170
92 atg gag ggc aca gtg gcg gcc cag gat gag ttc tac cgc agc ggc tgg 697
93 Met Glu Gly Thr Val Ala Ala Gln Asp Glu Phe Tyr Arg Ser Gly Trp
94                               175                               180                               185
96 gcc ctg aac atg aag gag ctg aag ctg ctg cag acc atc ggg aag ggg 745
97 Ala Leu Asn Met Lys Glu Leu Lys Leu Leu Gln Thr Ile Gly Lys Gly
98                               190                               195                               200
100 gag ttc gga gac gtg atg ctg ggc gat tac cga ggg aac aaa gtc gcc 793
101 Glu Phe Gly Asp Val Met Leu Gly Asp Tyr Arg Gly Asn Lys Val Ala
102 205                               210                               215                               220
104 gtc aag tgc att aag aac gac gcc act gcc cag gcc ttc ctg gct gaa 841
105 Val Lys Cys Ile Lys Asn Asp Ala Thr Ala Gln Ala Phe Leu Ala Glu
106                               225                               230                               235
108 gcc tca gtc atg acg caa ctg cgg cat agc aac ctg gtg cag ctc ctg 889
109 Ala Ser Val Met Thr Gln Leu Arg His Ser Asn Leu Val Gln Leu Leu
110                               240                               245                               250
112 ggc gtg atc gtg gag gag aag ggc ggg ctc tac atc gtc act gag tac 937
113 Gly Val Ile Val Glu Glu Lys Gly Gly Leu Tyr Ile Val Thr Glu Tyr
114                               255                               260                               265
116 atg gcc aag ggg agc ctt gtg gac tac ctg cgg tct agg ggt cgg tca 985
117 Met Ala Lys Gly Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser
118                               270                               275                               280
120 gtg ctg ggc gga gac tgt ctc ctc aag ttc tcg cta gat gtc tgc gag 1033
121 Val Leu Gly Gly Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu
122 285                               290                               295                               300
124 gcc atg gaa tac ctg gag ggc aac aat ttc gtg cat cga gac ctg gct 1081
125 Ala Met Glu Tyr Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala
126                               305                               310                               315
128 gcc cgc aat gtg ctg gtg tct gag gac aac gtg gcc aag gtc agc gac 1129

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RAW SEQUENCE LISTING

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DATE: 07/31/2006

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Input Set : A:\TSRI6516SEQ.TXT

Output Set: N:\CRF4\07312006\J535325.raw

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129 Ala Arg Asn Val Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp
130          320          325          330
132 ttt ggt ctc acc aag gag gcg tcc agc acc cag gac acg ggc aag ctg 1177
133 Phe Gly Leu Thr Lys Glu Ala Ser Thr Gln Asp Thr Gly Lys Leu
134          335          340          345
136 cca gtc aag tgg aca gcc cct gag gcc ctg aga gag aag aaa ttc tcc 1225
137 Pro Val Lys Trp Thr Ala Pro Glu Ala Leu Arg Glu Lys Lys Phe Ser
138          350          355          360
140 act aag tct gac gtg tgg agt ttc gga atc ctt ctc tgg gaa atc tac 1273
141 Thr Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Tyr
142 365          370          375          380
144 tcc ttt ggg cga gtg cct tat cca aga att ccc ctg aag gac gtc gtc 1321
145 Ser Phe Gly Arg Val Pro Tyr Pro Arg Ile Pro Leu Lys Asp Val Val
146          385          390          395
148 cct cgg gtg gag aag ggc tac aag atg gat gcc ccc gac ggc tgc ccg 1369
149 Pro Arg Val Glu Lys Gly Tyr Lys Met Asp Ala Pro Asp Gly Cys Pro
150          400          405          410
152 ccc gca gtc tat gaa gtc atg aag aac tgc tgg cac ctg gac gcc gcc 1417
153 Pro Ala Val Tyr Glu Val Met Lys Asn Cys Trp His Leu Asp Ala Ala
154          415          420          425
156 atg cgg ccc tcc ttc cta cag ctc cga gag cag ctt gag cac atc aaa 1465
157 Met Arg Pro Ser Phe Leu Gln Leu Arg Glu Gln Leu Glu His Ile Lys
158          430          435          440
160 acc cac gag ctg cac ctg tga cggctggcct ccgcctgggt catgggcctg 1516
161 Thr His Glu Leu His Leu *
162 445          450
164 tggggactga acctggaaga tcatggacct ggtgccccctg ctcaactgggc ccgagcctga 1576
165 actgagcccc agcgggctgg cgggcctttt tctgctgcc cagcctgcac ccctccggcc 1636
166 cgtctctct tggaccacc tgtggggcct ggggagccca ctgaggggcc agggaggaag 1696
167 gaggccacgg agcgggaggc agcggccac cacgtcgggc ttccctggcc tcccgccact 1756
168 cgccttctta gagttttatt cctttccttt tttgagattt ttttccgtg tgtttatttt 1816
169 ttattatttt tcaagataag gagaaagaaa gtaccagca aatgggcatt ttacaagaag 1876
170 tacgaatctt atttttctg tctgcccgt gaggggtgggg gggaccgggc ccctctctag 1936
171 ggacccctcg cccagcctc attccccatt ctgtgtccca tgtcccggtg ctccctcggtc 1996
172 gccccgtgtt tgcgcttgac catgttgac tgtttgcag cgcctgaggc agacgtctgt 2056
173 caggggcttg gatttcgtgt gccgtgcca cccgcccacc cgccttgta gatggaattg 2116
174 taataaacca cgccatgagg acaccgccc cgcctcggc gcttctcca ccgaaaaaaa 2176
175 aaaaaaaaaa a 2187
177 <210> SEQ ID NO: 2
178 <211> LENGTH: 450
179 <212> TYPE: PRT
180 <213> ORGANISM: homo sapiens
182 <400> SEQUENCE: 2
183 Met Ser Ala Ile Gln Ala Ala Trp Pro Ser Gly Thr Glu Cys Ile Ala
184 1 5 10 15
185 Lys Tyr Asn Phe His Gly Thr Ala Glu Gln Asp Leu Pro Phe Cys Lys
186 20 25 30
187 Gly Asp Val Leu Thr Ile Val Ala Val Thr Lys Asp Pro Asn Trp Tyr
188 35 40 45

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DATE: 07/31/2006

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Input Set : A:\TSRI6516SEQ.TXT

Output Set: N:\CRF4\07312006\J535325.raw

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189 Lys Ala Lys Asn Lys Val Gly Arg Glu Gly Ile Ile Pro Ala Asn Tyr
190      50      55      60
191 Val Gln Lys Arg Glu Gly Val Lys Ala Gly Thr Lys Leu Ser Leu Met
192 65      70      75      80
193 Pro Trp Phe His Gly Lys Ile Thr Arg Glu Gln Ala Glu Arg Leu Leu
194      85      90      95
195 Tyr Pro Pro Glu Thr Gly Leu Phe Leu Val Arg Glu Ser Thr Asn Tyr
196      100     105     110
197 Pro Gly Asp Tyr Thr Leu Cys Val Ser Cys Asp Gly Lys Val Glu His
198      115     120     125
199 Tyr Arg Ile Met Tyr His Ala Ser Lys Leu Ser Ile Asp Glu Glu Val
200      130     135     140
201 Tyr Phe Glu Asn Leu Met Gln Leu Val Glu His Tyr Thr Ser Asp Ala
202 145      150      155      160
203 Asp Gly Leu Cys Thr Arg Leu Ile Lys Pro Lys Val Met Glu Gly Thr
204      165      170      175
205 Val Ala Ala Gln Asp Glu Phe Tyr Arg Ser Gly Trp Ala Leu Asn Met
206      180     185     190
207 Lys Glu Leu Lys Leu Leu Gln Thr Ile Gly Lys Gly Glu Phe Gly Asp
208      195     200     205
209 Val Met Leu Gly Asp Tyr Arg Gly Asn Lys Val Ala Val Lys Cys Ile
210      210     215     220
211 Lys Asn Asp Ala Thr Ala Gln Ala Phe Leu Ala Glu Ala Ser Val Met
212 225      230      235      240
213 Thr Gln Leu Arg His Ser Asn Leu Val Gln Leu Leu Gly Val Ile Val
214      245      250      255
215 Glu Glu Lys Gly Gly Leu Tyr Ile Val Thr Glu Tyr Met Ala Lys Gly
216      260     265     270
217 Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser Val Leu Gly Gly
218      275     280     285
219 Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu Ala Met Glu Tyr
220      290     295     300
221 Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala Ala Arg Asn Val
222 305      310      315      320
223 Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp Phe Gly Leu Thr
224      325     330     335
225 Lys Glu Ala Ser Ser Thr Gln Asp Thr Gly Lys Leu Pro Val Lys Trp
226      340     345     350
227 Thr Ala Pro Glu Ala Leu Arg Glu Lys Lys Phe Ser Thr Lys Ser Asp
228      355     360     365
229 Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Tyr Ser Phe Gly Arg
230      370     375     380
231 Val Pro Tyr Pro Arg Ile Pro Leu Lys Asp Val Val Pro Arg Val Glu
232 385      390      395      400
233 Lys Gly Tyr Lys Met Asp Ala Pro Asp Gly Cys Pro Pro Ala Val Tyr
234      405     410     415
235 Glu Val Met Lys Asn Cys Trp His Leu Asp Ala Ala Met Arg Pro Ser
236      420     425     430
237 Phe Leu Gln Leu Arg Glu Gln Leu Glu His Ile Lys Thr His Glu Leu

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RAW SEQUENCE LISTING

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DATE: 07/31/2006

TIME: 14:19:29

Input Set : A:\TSRI6516SEQ.TXT

Output Set: N:\CRF4\07312006\J535325.raw

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238          435          440          445
239 His Leu
240          450
243 <210> SEQ ID NO: 3
244 <211> LENGTH: 4517
245 <212> TYPE: DNA
246 <213> ORGANISM: homo sapiens
248 <220> FEATURE:
249 <221> NAME/KEY: CDS
250 <222> LOCATION: (208)...(1839)
252 <400> SEQUENCE: 3
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254 gtcgcctatc ctgaccacag caaagcggcc cggagcccgc ggaggggacc tgacgggggc 120
255 gtaggcgccc gaaggctggg ggccccggag cggggccggc gtggcccagag ttccggtgag 180
256 cggacggcgg cgcgcgcaga tttgata atg ggc tgc att aaa agt aaa gaa aac 234
257                               Met Gly Cys Ile Lys Ser Lys Glu Asn
258                               1           5
260 aaa agt cca gcc att aaa tac aga cct gaa aat act cca gag cct gtc 282
261 Lys Ser Pro Ala Ile Lys Tyr Arg Pro Glu Asn Thr Pro Glu Pro Val
262 10          15          20          25
264 agt aca agt gtg agc cat tat gga gca gaa ccc act aca gtg tca cca 330
265 Ser Thr Ser Val Ser His Tyr Gly Ala Glu Pro Thr Thr Val Ser Pro
266          30          35          40
268 tgt ccg tca tct tca gca aag gga aca gca gtt aat ttc agc agt ctt 378
269 Cys Pro Ser Ser Ser Ala Lys Gly Thr Ala Val Asn Phe Ser Ser Leu
270          45          50          55
272 tcc atg aca cca ttt gga gga tcc tca ggg gta acg cct ttt gga ggt 426
273 Ser Met Thr Pro Phe Gly Gly Ser Ser Gly Val Thr Pro Phe Gly Gly
274          60          65          70
276 gca tct tcc tca ttt tca gtg gtg cca agt tca tat cct gct ggt tta 474
277 Ala Ser Ser Ser Phe Ser Val Val Pro Ser Ser Tyr Pro Ala Gly Leu
278          75          80          85
280 aca ggt ggt gtt act ata ttt gtg gcc tta tat gat tat gaa gct aga 522
281 Thr Gly Gly Val Thr Ile Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg
282 90          95          100          105
284 act aca gaa gac ctt tca ttt aag aag ggt gaa aga ttt caa ata att 570
285 Thr Thr Glu Asp Leu Ser Phe Lys Lys Gly Glu Arg Phe Gln Ile Ile
286          110          115          120
288 aac aat acg gaa gga gat tgg tgg gaa gca aga tca atc gct aca gga 618
289 Asn Asn Thr Glu Gly Asp Trp Trp Glu Ala Arg Ser Ile Ala Thr Gly
290          125          130          135
292 aag aat ggt tat atc ccg agc aat tat gta gcg cct gca gat tcc att 666
293 Lys Asn Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ala Asp Ser Ile
294          140          145          150
296 cag gca gaa gaa tgg tat ttt ggc aaa atg ggg aga aaa gat gct gaa 714
297 Gln Ala Glu Glu Trp Tyr Phe Gly Lys Met Gly Arg Lys Asp Ala Glu
298          155          160          165
300 aga tta ctt ttg aat cct gga aat caa cga ggt att ttc tta gta aga 762
301 Arg Leu Leu Leu Asn Pro Gly Asn Gln Arg Gly Ile Phe Leu Val Arg

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/535,325

DATE: 07/31/2006

TIME: 14:19:30

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